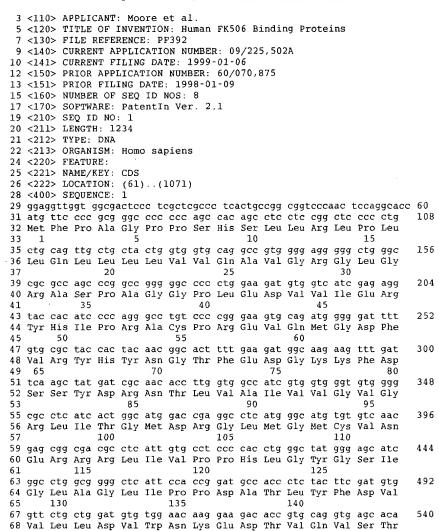```
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         PATENT APPLICATION: US/09/225,502A   TIME: 21:22:02

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P.5

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 3 <110> APPLICANT: Moore et al.
 5 <120> TITLE OF INVENTION: Human FK506 Binding Proteins
 7 <130> FILE REFERENCE: PF392
 9 <140> CURRENT APPLICATION NUMBER: 09/225,502A
10 <141> CURRENT FILING DATE: 1999-01-06
12 <150> PRIOR APPLICATION NUMBER: 60/070,875
13 <151> PRIOR FILING DATE: 1998-01-09
15 <160> NUMBER OF SEQ ID NOS: 8
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32 Met Phe Pro Ala Gly Pro Pro Ser His Ser Leu Leu Arg Leu Pro Leu
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35 ctg cag ttg ctg cta ctg gtg gtg cag gcc gtg ggg agg ggg ctg ggc  156
36 Leu Gln Leu Leu Leu Leu Val Val Gln Ala Val Gly Arg Gly Leu Gly
37               20                  25                  30
39 cgc gcc agc ccg gcc ggg ggc ccc ctg gaa gat gtg gtc atc gag agg  204
40 Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg
41           35                  40                  45
43 tac cac atc ccc agg gcc tgt ccc cgg gaa gtg cag atg ggg gat ttt  252
44 Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe
45       50                  55                  60
47 gtg cgc tac cac tac aac ggc act ttt gaa gat ggc aag aag ttt gat  300
48 Val Arg Tyr His Tyr Asn Gly Thr Phe Glu Asp Gly Lys Lys Phe Asp
49  65                  70                  75                  80
51 tca agc tat gat cgc aac acc ttg gtg gcc atc gtg gtg ggt gtg ggg  348
52 Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala Ile Val Val Gly Val Gly
53                  85                  90                  95
55 cgc ctc atc act ggc atg gac cga ggc ctc atg ggc atg tgt gtc aac  396
56 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
57              100                 105                 110
59 gag cgg cga cgc ctc att gtg cct ccc cac ctg ggc tat ggg agc atc  444
60 Glu Arg Arg Arg Leu Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
61          115                 120                 125
63 ggc ctg gcg ggg ctc att cca ccg gat gcc acc ctc tac ttc gat gtg  492
64 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val
65      130                 135                 140
67 gtt ctg ctg gat gtg tgg aac aag gaa gac acc gtg cag gtg agc aca  540
68 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln Val Ser Thr
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75 gtc cgc tac cac tac aat ggc acc ctg ctg gac ggc acc tcc ttc gac    636
76 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
77               180               185               190
79 acc agc tac agt aag ggc ggc act tat gac acc tac gtc ggc tct ggt    684
80 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
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83 tgg ctg atc aag ggc atg gac cag ggg ctg ctg ggc atg tgt cct gga    732
84 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
85      210               215               220
87 cag aga agg aag att atc atc cct cca ttc ctg gcc tat ggc gag aaa    780
88 Gln Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
89 225               230               235               240
91 ggc tat ggt gag ggt ggg caa gga cac aag ggg aaa ttc cgc aga aga    828
92 Gly Tyr Gly Glu Gly Gly Gln Gly His Lys Gly Lys Phe Arg Arg Arg
93               245               250               255
95 ggg aaa aac cag gcc tcc aca tac agt tgc tca ggt tgt ata ctg cac    876
96 Gly Lys Asn Gln Ala Ser Thr Tyr Ser Cys Ser Gly Cys Ile Leu His
97          260               265               270
99 gag ggc atc caa cca agg act caa ggt ggg atg aaa tct acc ctt ggt    924
100 Glu Gly Ile Gln Pro Arg Thr Gln Gly Gly Met Lys Ser Thr Leu Gly
101          275               280               285
103 gct act aag aag ggg tgc ttt ggc cgg gcg tgg tgg ctc acg ctt gta    972
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107 atc cca gca ctt tgg gaa gcc aag gcg gga gga tca cga ggt cca gga    1020
108 Ile Pro Ala Leu Trp Glu Ala Lys Ala Gly Gly Ser Arg Gly Pro Gly
109 305               310               315               320
111 gat cga gac cac ggt gaa acc ccg tct cta cta aaa ata caa aaa aat    1068
112 Asp Arg Asp His Gly Glu Thr Pro Ser Leu Leu Lys Ile Gln Lys Asn
113               325               330               335
115 tag ccgggcgtgg tgggggcgcc tgtagtccca gctactcgga gaggctgagg         1121
118 caggaaaatg acgtgaaccc gggaggcgga gcttgcagtg agccgagatc ttgccactgc 1181
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125 <212> TYPE: PRT
126 <213> ORGANISM: Homo sapiens
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132          20               25               30
133 Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg
134          35               40               45
135 Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe
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RAW SEQUENCE LISTING   DATE: 05/23/2000
PATENT APPLICATION: US/09/225,502A   TIME: 21:22:02

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05232000\I225502A.raw

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139 Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala Ile Val Val Gly Val Gly
140                  85                  90                  95
141 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
142                  100                 105                 110
143 Glu Arg Arg Arg Leu Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
144         115                 120                 125
145 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val
146         130                 135                 140
147 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln Val Ser Thr
148 145                 150                 155                 160
149 Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp Gly Asp Phe
150                  165                 170                 175
151 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
152                  180                 185                 190
153 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
154         195                 200                 205
155 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
156         210                 215                 220
157 Gln Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
158 225                 230                 235                 240
159 Gly Tyr Gly Glu Gly Gly Gln Gly His Lys Gly Lys Phe Arg Arg Arg
160                  245                 250                 255
161 Gly Lys Asn Gln Ala Ser Thr Tyr Ser Cys Ser Gly Cys Ile Leu His
162                  260                 265                 270
163 Glu Gly Ile Gln Pro Arg Thr Gln Gly Gly Met Lys Ser Thr Leu Gly
164         275                 280                 285
165 Ala Thr Lys Lys Gly Cys Phe Gly Arg Ala Trp Trp Leu Thr Leu Val
166         290                 295                 300
167 Ile Pro Ala Leu Trp Glu Ala Lys Ala Gly Gly Ser Arg Gly Pro Gly
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188 gtg agc aca ttg ctg cgc ccg ccc cac tgc ccc cgc atg gtc cag gac    97
189 Val Ser Thr Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp
190              20                  25                  30
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196 tcc ttc gac acc agc tac agt aag ggc ggc act tat gac acc tac gtc   193
197 Ser Phe Asp Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val
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200 ggc tct ggt tgg ctg atc aag ggc atg gac cag ggg ctg ctg ggc atg   241
201 Gly Ser Gly Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met
202  65                      70              75                  80
204 tgt cct gga gag aga agg aag att atc atc cct cca ttc ctg gcc tat   289
205 Cys Pro Gly Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr
206              85                      90                  95
208 ggc gag aaa ggc tat ggg aca gtg atc ccc cca cag gcc tcg ctg gtc   337
209 Gly Glu Lys Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala Ser Leu Val
210          100                     105                 110
212 ttt cac gtc ctc ctg att gac gtg cac aac ccg aag gac gct gtc cag   385
213 Phe His Val Leu Leu Ile Asp Val His Asn Pro Lys Asp Ala Val Gln
214          115                     120                 125
216 cta gag acg ctg gag ctc ccc ccc ggc tgt gtc cgc aga gcc ggg gcc   433
217 Leu Glu Thr Leu Glu Leu Pro Pro Gly Cys Val Arg Arg Ala Gly Ala
218          130                     135                 140
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221 Gly Asp Phe Met Arg Tyr His Tyr Asn Gly Ser Leu Met Asp Gly Thr
222 145                     150                 155             160
224 ctc ttc gat tcc agc tac tcc cac aac cac acc tac aat acc tat atc   529
225 Leu Phe Asp Ser Ser Tyr Ser His Asn His Thr Tyr Asn Thr Tyr Ile
226              165                     170                 175
228 ggg cag ggt tac atc atc ccc ggg atg gac cag ggg ctg cag ggt gcc   577
229 Gly Gln Gly Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu Gln Gly Ala
230              180                     185                 190
232 tgc atg ggg gaa cgc cgg aga att acc atc ccc ccg cac ctc gcc tat   625
233 Cys Met Gly Glu Arg Arg Arg Ile Thr Ile Pro Pro His Leu Ala Tyr
234          195                     200                 205
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237 Gly Glu Asn Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala Val Leu Ile
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241 Phe Asn Val His Val Ile Asp Phe His Asn Pro Ala Asp Val Val Glu
242 225                     230                 235             240
244 atc agg aca ctg tcc cgg cca tct gag acc tgc aat gag acc acc aag   769
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248 ctt ggg gac ttt gtt cga tac cat tac aac tgt tct ttg ctg gac ggc   817
249 Leu Gly Asp Phe Val Arg Tyr His Tyr Asn Cys Ser Leu Leu Asp Gly
250              260                     265                 270
252 acc cag ctg ttc acc tcg cat gac tac ggg gcc ccc cag gag gcg act   865
253 Thr Gln Leu Phe Thr Ser His Asp Tyr Gly Ala Pro Gln Glu Ala Thr
254          275                     280                 285
256 ctc ggg gcc aac aag gtg atc gaa ggc ctg gac acg ggc ctg cag ggc   913
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261 Met Cys Val Gly Glu Arg Arg Gln Leu Ile Val Pro Pro His Leu Ala
262 305             310             315             320
264 cac ggg gag agt gga gcc cgg gga gtc cca ggc agt gct gtg ctg ctg 1009
265 His Gly Glu Ser Gly Ala Arg Gly Val Pro Gly Ser Ala Val Leu Leu
266             325             330             335
268 ttt gag gtg gag ctg gtg tcc cgg gag gat ggg ctg ccc aca ggc tac 1057
269 Phe Glu Val Glu Leu Val Ser Arg Glu Asp Gly Leu Pro Thr Gly Tyr
270         340             345             350
272 ctg ttt gtg tgg cac aag gac cct cct gcc aac ctg ttt gaa gac ata 1105
273 Leu Phe Val Trp His Lys Asp Pro Pro Ala Asn Leu Phe Glu Asp Ile
274         355             360             365
276 gac ctc aac aag gat ggc gag gtc cct ccg gag gag ttc tcc acc ttc 1153
277 Asp Leu Asn Lys Asp Gly Glu Val Pro Pro Glu Glu Phe Ser Thr Phe
278     370             375             380
280 atc aag gct caa gtg agt gag ggc aaa gga cgc ctc atg cct ggg cag 1201
281 Ile Lys Ala Gln Val Ser Glu Gly Lys Gly Arg Leu Met Pro Gly Gln
282 385             390             395             400
284 gac cct gag aaa acc ata gga gac atg ttc cag aac cag gac cgc aac 1249
285 Asp Pro Glu Lys Thr Ile Gly Asp Met Phe Gln Asn Gln Asp Arg Asn
286             405             410             415
288 cag gac ggc aag atc aca gtc gac gag ctc aag ctg aag tca gat gag 1297
289 Gln Asp Gly Lys Ile Thr Val Asp Glu Leu Lys Leu Lys Ser Asp Glu
290             420             425             430
292 gac gag gag cgg gtc cac gag gag ctc tgagggcag ggagcctggc       1344
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316 ggaaccatag aagagaggaa gaaaacaaag ggcatgtgtg agggaagctg cttgggtggg 2004
318 tgttagggct atgaaatctt ggatttgggg ctgaggggtg ggagggaggg cagagctctg 2064
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327 <212> TYPE: PRT
328 <213> ORGANISM: Homo sapiens
330 <400> SEQUENCE: 4
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Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

VERIFICATION SUMMARY   DATE: 05/23/2000
PATENT APPLICATION: US/09/225,502A   TIME: 21:22:03

Input Set : A:\Pto.amc
Output Set: N:\CRF3\05232000\I225502A.raw

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L:622 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
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L:682 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:693 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:695 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:705 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:707 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:709 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:806 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:6
L:806 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:6
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